

Prevalence, risk factors, and molecular epidemiology of methicillin-resistant *Staphylococcus aureus* among newly arrested men in Baltimore, Maryland

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Background: Outbreaks of methicillin-resistant *Staphylococcus aureus* (MRSA) within prison populations seemingly attest to its spread within the corrections industry; however, the extent of MRSA colonization on arrest is unknown.

Methods: This study determined the prevalence and risk factors of *S aureus* on arrest. Nasal swabs from 602 newly arrested men were evaluated. Risk factors were assessed through self-report. Molecular characterization of each isolate was completed.

Results: The prevalence of *S aureus* nasal colonization was 40.4% (243/602). MRSA colonization was found in 15.8% (95/602) of the total population and in 39.1% (95/243) of the total *S aureus* isolates. Twenty-three skin infections were identified; of these, 11 (47.8%) were *S aureus* infections, with methicillin-susceptible *S aureus* (MSSA) in accounting for 3 cases (13.1%) and MRSA accounting for 8 cases (34.8%). In 2 cases (25%) of MRSA wound infection, the nasal colonizing strain was MSSA. By pulsed-field gel electrophoresis, 76 of 95 (80%) nasal isolates were found to be USA300 or related subtypes, with the other 19 (20%) being non-USA300 strains. The Pantone-Valentine leukocidin gene was identified in 38 (97.4%) USA300 isolates and in 6 (31.6%) non-USA 300 isolates.

Conclusion: MRSA colonization is far greater in this sample than in the general public. USA300 subtypes are highly prevalent. History of previous arrest was not associated with increased MRSA prevalence. MRSA risk factors differed significantly between those with and without a history of previous arrest. (Am J Infect Control 2008;36:644-50.)

Since the late 1990s, the emergence of community-associated methicillin-resistant *Staphylococcus aureus* (CA-MRSA) has been reported in numerous studies conducted in diverse community populations worldwide.¹⁻¹¹ In these studies, CA-MRSA was distinguished from nosocomial MRSA by distinct epidemiologic and molecular differences noted in the organisms, specifically USA300 pulsed-field gel electrophoresis (PFGE) strain type, presence of the Pantone-Valentine leukocidin (PVL) gene, and diminished antimicrobial resistance.¹² Over the last 5 years, new data on the evolving epidemiology of *S aureus* and CA-MRSA,^{11,13} as well as on the appearance and transmission of the organism in the health care setting,^{14,15} have blurred these distinctions.

Correctional facilities provide unique opportunities for both *S aureus* and MRSA transmission, and several outbreaks have been documented in recent years.¹⁶⁻¹⁸ Nonetheless, surveillance for MRSA colonization within correctional settings received little attention until a recent report by Lowy et al¹⁹ identified a 10.5% prevalence of MRSA colonization among prisoners in 2 New York State correctional institutions. Jail location was significantly associated with MRSA colonization in that study. The prevalence of MRSA colonization in prisoners undergoing hospitalization in a 13-bed correctional health unit at a large teaching hospital in Baltimore, Maryland was recently described by Wright et al.²⁰ In that study, the authors noted an overall nasal colonization prevalence of 11.5%, with a prevalence of 17.0% in individuals who had been transferred from a Baltimore City jail facility.

Based on these and other published data, we now have evidence of MRSA clinical infections inside prisons¹⁶⁻¹⁸ and knowledge that jail setting before incarceration may play a role in colonization.^{19,20} Further, a recent investigation in Chicago uncovered previous incarceration as a significant risk factor for MRSA clinical infections among persons hospitalized or receiving outpatient care.²¹ Collectively, these findings demonstrate the importance of active surveillance studies to detect MRSA colonization and/or infection at the time of arrest.

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The present study had 2 primary aims: (1) to determine the prevalence of methicillin-susceptible *S aureus* (MSSA) and MRSA nasal colonization and infection in men at the time of arrest and (2) to identify risk factors for acquisition of each pathogen. As a secondary aim, we investigated the phenotypic (ie, antimicrobial susceptibilities) and genotypic (ie, PFGE and PVL) characteristics of the isolates to determine whether the isolates were hospital-associated or community-associated. These data were presented in part at the 45th Annual Scientific Meeting of the Infectious Diseases Society of America (IDSA), San Diego, California, October 5, 2007.

METHODS

Study setting

The study was conducted in the Central Booking Intake Facility in Baltimore, MD from August to December 2006. Central Booking, the main intake center for persons arrested in Baltimore City, processes on average 175 new arrestees per day. The researcher was given access between 1 PM and 11 PM 5 days a week.

Subject selection

Subjects were eligible for participation by meeting the following criteria: arrested less than 24 hours before enrollment, male, age 21 years and older, and processed at the Central Booking Intake Facility in Baltimore. Female arrestees were excluded because of correctional staffing limitations.

Collection of clinical specimens

Anterior nasal specimens were obtained using BactiSwab II dual-headed culturettes (Remel, Lenexa, KS) from 602 of 678 men (89%) who were screened for participation and provided informed consent. Both swabs were inserted into each nostril at the same time. Wound specimens were obtained from 23 of these 602 men (3.8%). A single nurse practitioner collected all specimens. All swabs were transported at room temperature and stored at 5°C until processing within 24 hours of collection, which prevented supervised access to the subjects.

Risk factor evaluation

A standardized 50-item questionnaire was designed after reviewing the literature to identify factors that assessed a person's hospital and community risks for MRSA acquisition. The questionnaire also included basic demographic questions that were administered to each participating and nonparticipating subject as allowed. The jail screening medical record forms were

reviewed for clarity as needed. All questionnaire and medical record review was completed by the same nurse practitioner.

Microbiological evaluation

Using standard culture methods, a swab was streaked onto CHROMagar-MRSA (BD Diagnostics, Franklin Lakes, NJ), designated CHROM-MRSA hereinafter, a selective medium, and then placed in trypticase soy broth (TSB) with 6.5% NaCl.^{22,23} The CHROM-MRSA agar plates were incubated in the dark at 35°C and reviewed after 24 hours and again after 48 hours if necessary. Mauve-colored colonies were confirmed as *S aureus* by Gram's stain and slide coagulation or latex agglutination (Staphaurex + Remel).²⁴ Each TSB plate was subcultured after overnight incubation to 5% sheep's blood agar (SBA) plates (BBL; BD Diagnostics). The SBA plates were incubated aerobically for 24 to 48 hours at 35°C. Gram-positive cocci that were catalase-positive and slide coagulase-positive were identified presumptively as *S aureus*. If the matching CHROM-MRSA plates were negative, then the SBA isolates were subcultured to oxacillin screening agar (OSA) (BD Diagnostics) according to the manufacturer's protocol and read at 24 hours to determine methicillin susceptibility. Nasal and wound isolates growing on the CHROM-MRSA plates were considered to be MRSA; those isolates positive on OSA but not growing on the CHROM-MRSA plates were confirmed as gram-positive cocci in clusters, and identification and susceptibility testing was authenticated with the BD Phoenix Automated Microbiology System (BD Diagnostics).²⁵ Detection of the PVL gene was done as described by Lina et al.²⁶

Statistical analysis

Sample size was calculated using a conservative estimated MRSA prevalence of 2.5% ($\alpha = 0.05$; 80% power). The Student *t*-test or the χ^2 test was used for univariate analysis. Relative risk ratios (RRRs) and exact 95% confidence intervals (CIs) also were calculated using multinomial logistic regression, with likelihood ratio testing for model fit for each variable done independently. Variance inflation factors were evaluated for the presence of collinearity, with no evidence suggestive of such a finding. Once the final multinomial model was determined, each outcome (ie, MSSA and MRSA) was evaluated separately in multivariate logistic regression for the presence of interaction and confounding. All statistical analyses were done using Stata version 9.0 (StataCorp, College Station, TX).

The study design was approved by the Maryland Department of Corrections Research Committee, the Johns Hopkins University Institutional Review Board, and the Department of Health and Human Services

Office of Human Research Protections. A certificate of confidentiality was obtained from the National Institutes of Health to protect subjects from prosecution due to disclosure of sensitive risk factor information, such as self-reporting of intravenous drug use.

RESULTS

Demographics

A total of 678 persons were approached for participation. The enrolled sample comprised 602 arrested males, each of whom provided a nasal swab and wound culture if applicable. Demographic data also were collected on 67 of 75 (89.3%) persons who declined to participate but agreed to collection of demographic information. The remaining 8 subjects refused any participation. Demographic characteristics of the 2 groups were compared to evaluate bias in sample selection. The 2 samples were equivalent with regard to race, health status, and residence (Baltimore City vs other location). Educational status differed between the groups, with a higher level of educational preparation (ie, some college or higher) among those who refused to participate (26.9% vs 18.3%; $P = .003$). Among the study participants, differences in age and health status were identified in the 3 possible culture outcomes (Table 1).

Prevalence of and risk factors for *S aureus* colonization

During the study period, the prevalence of *S aureus* nasal colonization in this cohort was 40.4% (243/602); 15.8% (95/602) of the overall cohort was colonized with MRSA, representing 39.1% (95/243) of the *S aureus* isolates. Univariate analysis revealed several differences between the men with and without *S aureus* colonization. The men with *S aureus* colonization were older ($P = .009$) and more likely to report the following: fair/poor health ($P = .043$), chronic skin disease ($P = .017$), active intravenous drug use ($P = .046$), and history of abscess ($P = .007$). Differences in race, location of residence (ie, Baltimore City vs other location), self-described health status, or education were not statistically significant between the men with and without *S aureus* colonization (Table 2).

Bivariate multinomial logistic evaluation of risk associated with *S aureus* colonization (excluding MRSA) identified arrestees who reported a history of abscess as significantly more likely to harbor MSSA (Table 3). Those with MSSA colonization were more likely to be Caucasian and also more likely to report fair/poor health. Despite literature reports of increased *S aureus* colonization in athletes,⁵ those healthy enough for routine sports participation were protected against MSSA

colonization in this cohort. A history of previous arrest was not associated with MSSA colonization.

Among those with MRSA colonization, the prevalence was greatest in those age 30 to 49 years (Table 3). Similar to the men colonized with MSSA, those colonized with MRSA reported a higher incidence of fair/poor health and history of abscess. Additional factors associated specifically with MRSA colonization included reports of chronic skin disease, antibiotic use in the last 6 months, current abscess at the time of arrest, and active intravenous drug use in the last 6 months.

When we evaluated the multivariate multinomial regression analysis of *S aureus* colonization, Caucasian race (RRR = 1.99; 95% CI = 1.22 to 3.29; $P = .006$) and history of abscess (RRR = 1.83; 95% CI = 1.06 to 3.16; $P = .00$) remained significant. As in MSSA, a history of abscess was strongly associated with MRSA colonization in this group (RRR = 2.91; 95% CI = 1.62 to 5.22; $P = .00$). In addition, men age 30 to 49 years were more likely to be colonized with MRSA (RRR = 2.68; 95% CI = 1.48 to 4.84; $P = .001$).

Approximately 40% ($n = 243$) of the cohort reported a history of previous arrest within the 6 months preceding the current arrest. When the sample was stratified between persons with and without a history of previous arrest, several interesting differences were noted. Men colonized with MRSA but without a history of previous arrest maintained the same exact risk factors noted earlier (ie, history of abscess and age 30 to 49 years). Men with a history of previous arrest also were noted to have several additional risk factors, 2 of which were directly associated with previous incarceration activities (Table 4).

S aureus skin and soft tissue infections

The enrolled subjects reported a total of 23 skin and soft tissue infections. *S aureus* infection was noted in 11 of these cases (47.8%); of these 11 cases, MSSA was isolated in 3 (13.1%) and MRSA was isolated in 8 (34.8%). Of the 8 MRSA-infected wounds, 5 (62.5%) were colonized with the infecting MRSA strain. In 2 subjects (25%), the nasal colonizing strain was MSSA; 1 subject exhibited no nasal colonization.

Molecular characterization of MRSA isolates

By PFGE, 76 of 95 nasal isolates (80%) were identified as USA300 or related subtypes; the remaining 19 isolates (20%) were non-USA300 strains. No USA 400 isolates were identified. Among the wound isolates, 5 of the 8 (62.5%) MRSA isolates were USA300 strains.

Polymerase chain reaction (PCR) was performed on a 50% sample of USA300 and all non-USA300 isolates to detect the PVL gene. This gene was identified in 38

Table 1. Demographic characteristics of new arrestees with and without *S aureus* colonization

Baseline demographics	<i>S aureus</i> -negative (n = 359), n (%)	MSSA (n = 148), n (%)	MRSA (n = 95), n (%)	P value*
Age, years				
21 to 29	120 (33.4)	39 (26.4)	17 (17.9)	.009
30 to 49	192 (53.5)	89 (60.1)	70 (73.7)	
50+	47 (13.1)	20 (13.5)	8 (8.4)	
Race				
African American, non-Hispanic	286 (79.7)	102 (68.9)	69 (72.6)	.088
Caucasian, non-Hispanic	51 (14.2)	35 (23.7)	20 (21.1)	
Other	22 (6.1)	11 (7.4)	6 (6.3)	
ZIP code of residence				
Baltimore City	307 (85.5)	116 (78.4)	83 (87.4)	.086
Other	52 (14.5)	32 (21.6)	12 (12.6)	
Education				
Did not finish high school	124 (34.5)	48 (32.4)	34 (35.8)	.344
High school graduate	162 (45.1)	78 (52.7)	46 (48.4)	
Some college	62 (17.3)	15 (10.1)	11 (11.6)	
College graduate	11 (3.1)	7 (4.7)	4 (4.2)	
Health status				
Excellent or good	244 (67.9)	87 (58.8)	54 (56.8)	.043
Fair or poor	115 (32.1)	61 (41.2)	41 (43.2)	

Significant P values are in bold.

*Chi-squared analysis.

Table 2. Comparison of self-reported risk factors by culture outcome within 6 months of arrest

	<i>S aureus</i> -negative, n (%)	MSSA, n (%)	MRSA, n (%)	P value
Admitted to hospital	71 (19.8)	24 (16.2)	25 (26.3)	.156
Smoking	263 (73.3)	103 (69.6)	75 (78.9)	.275
Chronic skin disease	29 (8.1)	14 (9.5)	17 (17.9)	.017
Chronic steroid use	10 (2.8)	4 (2.7)	1 (1.1)	.617
Chronic injectable medication	5 (1.4)	4 (2.7)	2 (2.1)	.591
Intravenous drug user	51 (14.2)	29 (19.6)	23 (24.2)	.046
HIV-positive	17 (4.7)	9 (6.1)	4 (4.2)	.762
Antibiotics for any reason	72 (20.1)	32 (21.6)	29 (30.5)	.090
Household member arrested	49 (13.7)	14 (9.5)	15 (15.8)	.296
Sports participation	85 (23.7)	23 (15.5)	19 (20.0)	.119
Use of gym facility	21 (5.6)	9 (6.1)	8 (8.4)	.651
Physical altercation	56 (15.6)	19 (12.8)	20 (21.1)	.228
Child in daycare	158 (44.0)	54 (36.5)	35 (36.8)	.195
Household member in hospital	46 (12.8)	21 (14.2)	12 (12.6)	.906
Current abscess	16 (4.5)	9 (6.1)	10 (10.5)	.079
Previous abscess	32 (8.9)	22 (14.9)	19 (20.0)	.007
Household abscess	20 (5.6)	14 (9.5)	8 (8.4)	.246
Previous arrest	148 (41.2)	58 (39.2)	37 (38.9)	.872
Sexual contact	290 (80.8)	118 (79.7)	78 (82.1)	.900
Sex with commercial sex worker	19 (5.3)	12 (8.1)	3 (3.2)	.238

Significant P values are in bold.

* χ^2 analysis.

of 39 (97.4%) USA300 and related strains, in 6 of 19 (31.6%) non-USA 300 isolates, and in 7 of 60 (11.7%) *S aureus* isolates evaluated. The results of in vitro susceptibility testing, presented in Table 5, showed a > 95% susceptibility to trimethoprim-sulfamethoxazole (Bactrim) as well as a high discordance between clindamycin and erythromycin susceptibility, suggesting the need to confirm the presence of in vitro

inducible macrolide-lincosamide-streptogramin B resistance (iMLS) (D-test) analysis in this patient population.²⁷

DISCUSSION

This is the first surveillance study to investigate *S aureus* and MRSA colonization at the time of arrest to

Table 3. Results of bivariate multinomial logistic regression for *S aureus* colonization of new arrestees

	RRR	95% CI	P value
Risk factors for MSSA colonization			
African American versus Caucasian	1.92	1.18 to 3.13	.008
Fair/poor health	1.22	1.00 to 1.49	.049
Sports participation	0.59	0.36 to 0.98	.043
History of abscess (current/previous)	1.78	1.05 to 3.03	.033
Risk factors for MRSA colonization			
Age 30 to 49 years	2.57	1.45 to 4.58	.001
Fair/poor health	1.27	1.01 to 1.60	.043
Chronic skin disease	2.48	1.30 to 4.74	.006
Antibiotic use in last 6 months	1.75	1.05 to 2.91	.030
Current abscess on arrest	2.52	1.11 to 5.76	.028
History of abscess (current/previous)	2.84	1.62 to 4.99	.000
Intravenous drug use in last 6 months	1.93	1.11 to 3.36	.020

All risk factors listed in Table 2 were included in the model; only significant Findings are presented here.

Table 4. Risk factors for MRSA colonization in men with a previous arrest history (n = 243; MRSA prevalence, 15.2%)

	RRR	95% CI	P value
Age 30 to 49 years	4.10	1.47 to 11.43	.007
Hospital admission within 6 months of arrest	2.91	1.22 to 6.93	.016
Household abscess within 6 months of arrest	3.95	1.00 to 15.56	.049
Skin infection during previous incarceration	9.15	1.77 to 47.20	.008
Use of prison weight room/gym during previous incarceration	4.48	1.20 to 17.20	.029

identify the prevalence and risk profiles of persons entering a large city jail system. The prevalences of both *S aureus* (40.4%) and MRSA (15.8%) among nasal isolates were substantially greater than those estimated from the largest and most representative community analysis of the prevalence of MRSA colonization conducted to date, which noted *S aureus* and MRSA colonization prevalences of 31% and 0.84%, respectively.²⁸ Our findings also reveal a higher prevalence of colonization than was found in New York prisoners who were already serving their sentences,¹⁹ which may represent a regional difference or demonstrate a higher prevalence among newly arrested persons compared with incarcerated individuals. Our findings are similar to the prevalence noted on hospitalization of prisoners originating from Baltimore City jail facilities (15.8% vs 11.5%),²⁰ demonstrating a high prevalence of CA-MRSA in Baltimore; however, these data do not necessarily support acquisition in the jail setting, given the similarities in prevalence.

Interestingly, the present study found no difference in the prevalence among those with and without

Table 5. Antimicrobial susceptibilities of *S aureus* isolates

	Susceptibility, %		
	MRSA USA 300 (n = 76)	MRSA non-USA 300 (n = 19)	MSSA (n = 148)
Erythromycin	10.5	63.2	71.6
Clindamycin	88.2	94.7	96.6
Gentamicin	98.7	89.5	100.0
Moxifloxacin	10.5	63.2	100.0
Nitrofurantoin	100.0	100.0	100.0
Oxacillin	0.0	15.8	100.0
Rifampin	100.0	100.0	100.0
Tetracycline	97.4	84.2	98.6
Trimethoprim-sulfamethoxazole	97.4	84.2	97.3
Vancomycin	100.0	100.0	100.0

Non-USA 300 includes USA 100, 500, 700 and unique strains.

previous arrest (16.2% vs 15.2%). This finding is noteworthy given recent reports of an increased risk of clinical infection in persons who were previously incarcerated,²¹ and it may speak to recent data suggesting that nasal colonization with MRSA is not a necessary antecedent to CA-MRSA infection.²⁹ Notably, 2 (25%) of the subjects with clinical wound infections in this study were colonized with MSSA. Data are emerging on the need to culture other anatomic sites besides the nares (ie, groin, rectum, and axillae) to obtain a true picture of CA-MRSA colonization.³⁰ The exclusive nares culturing may be a limitation of this study.

Despite a similar prevalence in those with and without a history of previous arrest, the risk factors for MRSA colonization were strikingly different in the 2 groups. The men with no history of previous arrest exhibited characteristics consistent with the overall sample. Those reporting a previous arrest were significantly more likely to be colonized with MRSA if they routinely used the gym/weight room or had a skin infection during their previous incarceration. These correctional-specific risk factors provide insight into the mechanisms of transmission within correctional facilities.

USA300 PFGE subtypes and the PVL gene are molecular factors that have been identified as markers of CA-MRSA.¹² The present study reveals that most of the MRSA isolates identified in this sample, and thus entering the jail, were USA300 or related subtypes (76/95; 80%), with phenotypic characteristics suggesting acquisition within the community. Risk factor analysis of this data set did not identify any significant hospital-associated MRSA risk factors, again supporting community acquisition.

The present study identifies the burden faced by a correctional agency when attempting to limit intrafacility transmission due to the continual entrance of

colonized and infected individuals capable of transmitting MRSA. The booking process is often slow and tedious, leading to long backlogs of arrestees waiting in overcrowded holding cells. Isolation cells for persons with known draining or open wounds typically are not available.⁵¹ These conditions are likely antecedents to the occurrence of a future outbreak of skin and soft tissue infections related to CA-MRSA. Evidenced-based infection control interventions are needed in these settings to limit such transmission.

Recently published mathematical modeling of an outbreak of CA-MRSA in the Los Angeles County Jail⁵² provides insight into the hypothesis of community burden affecting jail transmission. That report identifies the continual entry of newly arrested individuals colonized or infected with MRSA as the primary mechanism sustaining the outbreak. The analysis elegantly demonstrates the derivation of the reproduction number (R_0), the average number of secondary infections generated by a single infectious case. The model likely overestimates community-associated prevalence by including cultures obtained up to 5 days after arrest as part of admission screening. Nevertheless, this model provides a useful tool for characterizing the extent of intrafacility transmission.

The participation rate in our study of 89% was higher than expected. We believe that this is likely due to current community knowledge of the primary clinical consequences of this bacterium, so-called “spider bites” or “boils.” Many participants reported having or knowing a person recently having these. All participants were advised that participation was not mandatory. Furthermore, we attempted to control for selection bias in this study by consistently offering enrollment to all arrestees as part of their medical screening. Nonetheless, it is possible that persons with a known history of MRSA or active skin infection were more likely to refuse participation in the study to avoid being identified. We believe that it is unlikely that the participants became colonized with MRSA during the arrest process, because they generally were handcuffed while being transported, precluding the potential for hand-to-nose contact. There may be differences in the colonization rate among persons arrested and processed before 1 PM and those done so after 11 PM, although arrests occurred at random throughout the city. Finally, our study was unable to recruit female arrestees, limiting the generalizability of our data beyond male arrestees. Female inmates have been shown to have a higher frequency of MRSA colonization in several studies;^{17,19,53} therefore, their inclusion may have increased the overall MRSA prevalence in this study. The overall burden of MRSA among new arrestees as a population is likely to be greater than our current estimate.

Our findings have broad implications for correctional settings. The prevalence of MRSA in men at the time of arrest is much higher than that in the general population. Infection control professionals and other correctional health personnel must consider *S aureus* and MRSA an ongoing threat to the health and well being of the inmate population and correctional staff. Risk reduction strategies targeting the prevention of future outbreaks are needed in both the jail and prison settings. Evaluation of low-cost prevention strategies within the correctional environment is an urgently needed area of future research.

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