Increasing Prevalence of Methicillin-Resistant Staphylococcus aureus Infection in California Jails

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Staphylococcus aureus clinical isolates obtained from patients who were inmates of the San Francisco County jail system showed an increase in the prevalence of methicillin-resistant Staphylococcus aureus (MRSA) from 29%, in 1997, to 74%, in 2002; 91% of the MRSA isolates carried staphylococcal chromosomal cassette mec (SCCmec) type IV. Pulsed field gel electrophoresis and multilocus sequence typing demonstrated 2 major clonal groups. One of these clonal groups is genetically indistinguishable from the strain responsible for an outbreak of MRSA in the Los Angeles County jail system in 2002.

Methicillin-resistant Staphylococcus aureus (MRSA) infections have traditionally been associated with health care facilities and are linked to well-defined risk factors [1]. Recently, MRSA epidemiology seems to be changing. Numerous case series, anecdotal reports, and epidemiological studies have described MRSA isolates from patients with community-acquired MRSA (CA-MRSA) infections who lack health care–associated risk factors [2–5]. Two recent reports from the Centers for Disease Control (CDC; Atlanta, GA) described large outbreaks of MRSA infection among incarcerated persons in a Mississippi state prison [6] and in Los Angeles County jails [7]. We report here the prevalence and distribution of MRSA genotypes and staphylococcal chromosomal cassette mec (SCCmec) types among clinical isolates obtained from jail inmates in San Francisco County over a 6-year period between 1997 and 2002.

Methods. Retrospective data collection was approved by the Committee on Human Research, Office of Research Administration, at the University of California, San Francisco. A retrospective review was conducted of the electronic records for all cultures positive for S. aureus that originated from jailed patients and that were performed between January 1997 and December 2002 in the San Francisco General Hospital (SFGH) Clinical Microbiology Laboratory. This laboratory receives specimens from the San Francisco Community Health Network (CHN), which includes Jail Health Services (consisting of 5 jails and a jail hospital ward), San Francisco General Hospital and its associated clinics, and 11 satellite community clinics. Aside from the specimen source, patient location, collection date, sex, and age of the patient, no clinical information was accessible.

S. aureus isolates were tested for phenotypic resistance to oxacillin by the salt agar method [8], and the presence of the mecA gene was confirmed by PCR [9]. Susceptibility to ciprofloxacin, tetracycline, gentamicin, erythromycin, cotrimoxazole, rifampin, clindamycin, and vancomycin was tested using microbroth dilution with the MicroScan WalkAway 96 instrument (Dade Behring), and the results were interpreted in accordance with the NCCLS guidelines (M7-A5) [10].

PFGE using the restriction enzyme Smal was performed as described elsewhere [11] and was interpreted according to Tenover [12]. Two representative isolates from the PFGE groups that included >1 isolate were further characterized by multilocus sequence typing (MLST) to define their MRSA clonal group, in accordance with the MLST database (available at http://www.mlst.net) [13]. Each clonal group in this study is designated by the combination of MLST sequence type and PFGE group (e.g., “ST30:Z”). SCCmec type was identified using a PCR-based protocol described elsewhere [9]. Annual prevalence of MRSA among patients in jails was calculated. Only 1 isolate per patient per year was included in the analysis. Fisher’s exact test was used to test for a significant trend [14].

Results. Of the 295 individuals (225 men and 70 women) with cultures positive for S. aureus, 158 (54%) had isolates that were MRSA. Of 158 MRSA isolates, 134 (85%) were recovered from wounds or soft-tissue samples, 7 (4%) from urine samples, 5 (3%) from blood samples, 5 (3%) from samples obtained
The 151 MRSA isolates available for genotyping were differentiated into 12 distinct MLST:PFGE clonal groups, 6 containing multiple isolates and 6 containing unrelated isolates. Four PFGE clonal groups (ST30:Z, ST8:S, ST8:C, and ST59:P) accounted for 89% of isolates (134 of 151 isolates). The ST30:Z clonal group initially comprised 33% of all MRSA isolates, in 1997, and increased in prevalence until it peaked at 54% of all MRSA isolates (22 of 41), in 2000 (figure 1). In 2001, the prevalence of this ST30:Z clonal group decreased to 33% of MRSA strains (9 of 27), and a new clonal group, ST8:S, appeared, accounting for 41% of MRSA isolates (11 of 27). By 2002, the ST8:S clonal group had increased in prevalence to 67% of all strains isolated from jailed patients (29 of 43 isolates) (figure 1). No association between clonal group and either specimen type or jail location was noted.

Antimicrobial resistance patterns by clonal group are shown in table 1. Twelve percent of all MRSA isolates (18 of 151) were multidrug-resistant (i.e., were resistant to ≥3 non–β-lactam antibiotics). Four of the 7 ST5:D isolates and 2 of the 6 unrelated clones were classified as multidrug-resistant MRSA. Only ST5:D and ST8:S showed a high proportion of resistance to ciprofloxacin (5 [71%] of 7 and 29 [72%] of 40 isolates, respectively). Sixty-four percent of all clones (96 of 151) were resistant to erythromycin, including 95% of ST8:S clones (38 of 40).

Of the 151 isolates typed, 91% (137 of 151) were SCCmec type IV (table 2). SCCmec type II was found in 5% of isolates (7 of 151) and was only associated with the ST5:D clonal group. SCCmec type III was found in 2 isolates of the ST59:P clonal group and in 1 unrelated isolate. Four isolates had profiles that were different from previously described SCCmec types I–IV, and they were present in the ST72:B and ST30:Z clonal groups. SCCmec type IV was seen consistently over the study period and was found in all major clonal groups except ST5:D. Nine percent of isolates with SCCmec type IV (12 of 137) were multidrug-resistant MRSA.

Discussion. This is the first longitudinal study of MRSA infection in a jail setting. In contrast to the 2 reports of MRSA outbreaks in correctional facilities [6, 7], this study provides a description of trends in the prevalence and distribution of MRSA clonal groups among an incarcerated population. Over the 6-year period from 1997 to 2002, MRSA prevalence increased or remained steady in every year except 1999. Jail health clinicians could identify no changes in the patient population or the jail environment that would account for the decrease in 1999 (J. Goldenson, personal communication). By 2001–2002, the prevalence of MRSA infection in jails appears to have plateaued at ~75% of S. aureus infections, a level significantly greater than its prevalence among nosocomial (48%) and com-

![Figure 1](https://example.com/figure1.png)

**Figure 1.** Annual distribution of MRSA in isolates obtained from the population of the San Francisco County jail system. The line graph indicates the percentage of MRSA among all S. aureus isolates. The bar graph indicates the proportions of MRSA isolates associated with different clonal groups. For an explanation of the clonal group designations, see Methods. An isolate is classified as “unique” if it has a PFGE profile unrelated to that of any other isolate.
Table 1. Antimicrobial resistance of clonal groups of methicillin-resistant Staphylococcus aureus (MRSA) isolates from jail inmates in San Francisco.

<table>
<thead>
<tr>
<th>Clonal groupa</th>
<th>No. of isolates</th>
<th>Proportion of isolates with drug resistance, by drug</th>
</tr>
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<tbody>
<tr>
<td></td>
<td>Gen</td>
<td>Cip</td>
</tr>
<tr>
<td>ST30:Z</td>
<td>57</td>
<td>0</td>
</tr>
<tr>
<td>ST8:S</td>
<td>40</td>
<td>0</td>
</tr>
<tr>
<td>ST8:C</td>
<td>19</td>
<td>0</td>
</tr>
<tr>
<td>ST59:P</td>
<td>18</td>
<td>0</td>
</tr>
<tr>
<td>ST5:D</td>
<td>7</td>
<td>1 (14)</td>
</tr>
<tr>
<td>ST72:B</td>
<td>4</td>
<td>0</td>
</tr>
<tr>
<td>Uniqueb</td>
<td>6</td>
<td>1 (17)</td>
</tr>
<tr>
<td>Total, % (no.)</td>
<td>151</td>
<td>2 (1)</td>
</tr>
</tbody>
</table>

**NOTE.** Data are no. of isolates (% of isolates in the specified clonal group), unless otherwise indicated. A multidrug-resistant (MDR) isolate is defined as an MRSA isolate resistant to ≥3 non-β-lactam antibiotics. Cip, ciprofloxacin; Cli, clindamycin; Ery, erythromycin; Gen, gentamicin; Rif, rifampin; Tcn, tetracycline; Tms, trimethoprim-sulfamethoxazole.

* For an explanation of the clonal group designations, see Methods.

b An isolate is classified as “unique” if it has a PFGE profile unrelated to that of any other isolates.

Community-acquired (36%) MRSA infection in San Francisco’s CHN during the same time period (F.P.R., unpublished data). This value is also greater than the 67% prevalence of MRSA infections reported by the National Nosocomial Infections Surveillance system for intensive care units [15]. This dramatic increase in the prevalence of MRSA infections among jailed patients is significant because it represents changes in a unique population in an institutionalized setting outside the locales in which health care–associated or community-associated MRSA infection is traditionally present.

The increase in the prevalence of MRSA infections over this 6-year period is largely attributable to 2 clonal groups: ST30:Z and ST8:S (figure 1). These 2 groups account for 64% of the MRSA isolates obtained, with ST30:Z predominating prior to 2000 and ST8:S predominating in 2001–2002. The ST8:C clonal group showed a general decline in prevalence over the survey period, and the distributions among the remaining 3 major clonal groups showed no temporal patterns. According to our retrospective data collection, the ST8:S clonal group was first noted in September 2000, when it was identified from a culture obtained from an outpatient with a skin and soft-tissue infection. It was subsequently noted 9 months later in an isolate obtained from a hospitalized patient (F.P.R., unpublished data). It is interesting that the ST8:S and ST8:C clonal groups are indistinguishable by MLST but possess distinct PFGE profiles (i.e., a >6-band difference). Thus, the genomic relationship between the ST8:S and ST8:C clonal groups needs to be explored further.

The ST8:S strain is not unique to San Francisco. Its clonal profile, according to PFGE, MLST, and spa typing, is consist-
tent with that of the predominant strain of MRSA that was common to a series of CA-MRSA outbreaks reported in Los Angeles in 2002 (F.P.R., unpublished data). The CDC stated in a recent report [7] that this PFGE pattern was also seen in a strain causing community outbreaks elsewhere in the United States; thus, this clone apparently has widespread geographic distribution.

Four of the 6 major clonal groups identified among this jail population (ST30:Z, ST8:S, ST8:C, and ST5:D) belong to 3 of the 5 globally disseminated epidemic MRSA clonal complexes (CC30, CC8, and CC5) [16]. The other 2 major clonal groups, ST59:P and ST72:B, have not previously been associated with MRSA clonal complexes. The major MRSA clonal groups detected in this study are genetically unrelated to the recently sequenced epidemic strain MW2 [5, 17]. MW2 belongs to the ST1 clonal group and carries SCCmec type IV. The presence of SCCmec type IV in multiple clonal groups identified in this article and elsewhere [18–21] further demonstrates that the SCCmec type IV element is carried in diverse genomes. It also supports the theory that SCCmec type IV may be more mobile and more easily transferred laterally between diverse S. aureus genomes than was previously thought, and thus may play a role in the success of these clones [21].

In contrast to previous reports characterizing CA-MRSA SCCmec type IV strains as typically not being multidrug-resistant [19, 20], in our study, 9% of the CA-MRSA SCCmec type IV strains (including 11 of 40 ST8:S isolates) were multidrug-resistant. Moreover, 72% of ST8:S strains in our study, as well as all 5 reference strains obtained from the recent Los Angeles outbreaks, are resistant to ciprofloxacin [7]. The finding of multidrug-resistant strains in the newly emergent and rapidly expanding ST8:S clonal group is cause for concern.

This report reflects the importance of MRSA infections that occur outside of traditional health care settings, and it identifies a high prevalence, as well as a potential reservoir, of MRSA infections in correctional facilities. Although the study was limited by its reliance on retrospective data collection and by a lack of information regarding the potential confounding risk factors and the clinical significance of the specimens, it illustrates the need for further investigation regarding risk factors, effective preventive strategies, and appropriate interventions in jail facilities to minimize further transmission into the community. Additional studies investigating the role of S. aureus virulence factors and their association with clinical disease are currently under way.

Acknowledgments

We thank Nick Moss, for his assistance with the laboratory work, and Dr. Joe Goldenson, Medical Director of San Francisco Jail Health Services, for his clinical insight into the population of the San Francisco County jail system. We would also like to thank Dr. Sydney M. Harvey, Los Angeles Department of Health Services, for sharing the 5 strains of S. aureus obtained during the Los Angeles jail outbreaks in November 2002.

References

