Molecular Evidence for Spread of Two Major Methicillin-Resistant *Staphylococcus aureus* Clones with a Unique Geographic Distribution in Chinese Hospitals

Yudong Liu,1, 2 Hui Wang,1, 2,* Na Du,3 Enhua Shen,3 Hongbin Chen,1, 2 Junqi Niu,3 Huifen Ye,4 and Minjun Chen1

Department of Clinical Laboratory, Peking Union Medical College Hospital, Chinese Academy of Medical Sciences, Beijing 100730, People’s Republic of China1; Graduate School, Peking Union Medical College, Chinese Academy of Medical Sciences, Beijing 100730, People’s Republic of China2; Department of Infectious Diseases, First Affiliated Hospital of Bethune Medical College, Jilin University, Changchun 130021, People’s Republic of China2; and Department of Clinical Laboratory, Guangzhou First Municipal People’s Hospital, Guangzhou 510180, People’s Republic of China4

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Methicillin (meticillin)-resistant *Staphylococcus aureus* (MRSA) is a serious problem worldwide. To investigate the molecular epidemiology of MRSA isolates in China, a total of 702 MRSA isolates collected from 18 teaching hospitals in 14 cities between 2005 and 2006 were characterized by antibiogram analysis, pulsed-field gel electrophoresis (PFGE), staphylococcal cassette chromosome mec (SCCmec) typing, and spa typing; and 102 isolates were selected for multilocus sequence typing (MLST). Overall, SCCmec type III was the most popular type and was found in 541 isolates (77.1%), followed by SCCmec type II (109/702; 15.5%). Twenty-four PFGE types were obtained among 395 isolates collected in 2005, and 18 spa types were obtained among 702 isolates. spa type t030, which corresponded to PFGE types A to E, constituted 52.0% (365/702) of all isolates, and isolates of this type were present in all 14 cities; spa type t037, which corresponded to PFGE types F and G, accounted for 25.5% (179/702) of all isolates, and isolates of this type were identified in 12 cities. The two spa genotypes belonged to sequence type 239 (ST239) and carried SCCmec type III. spa type t002, which included isolates of PFGE types L to T, made up 16.0% (112/702) of the isolates that belonged to ST5 and SCCmec type II, and isolates of this type were distributed in 12 cities. The distribution of spa types varied among the regions. spa type t002 was the most common in Dalian (53.4%) and Shenyang (44.4%); spa type t037 was predominant in Shanghai (74.8%), whereas spa type t030 was the most common in the other cities. Two isolates from Guangzhou that harbored SCCmec type IVa with ST59 and ST88 were identified as community-associated MRSA. The prevalence of the Panton-Valentine leukocidin gene was 2.3%. The data documented two major epidemic MRSA clones, ST239-MRSA-SCCmec type III and ST5-MRSA-SCCmec type II, with unique geographic distributions across China.

The emergence and spread of multidrug-resistant clones of methicillin (meticillin)-resistant *Staphylococcus aureus* (MRSA) are worldwide problems (7, 17). The recent emergence of highly virulent community-associated MRSA (CA-MRSA) strains and vancomycin-resistant, intermediate-resistant, or heteroresistant S. aureus strains further heightens public health concerns (3, 16, 20, 26, 29). According to a study conducted in 2005, the mean incidence of MRSA across China was over 50%, and in Shanghai, the prevalence was over 80% (30). Therefore, understanding and controlling the spread of MRSA in both hospital and community settings are now of paramount importance.

One of the efficient ways of controlling the spread of MRSA is through determination of the genotypic characteristics of MRSA clones as well as the genetic relatedness of the strains in different geographic regions (7, 10). Pulsed-field gel electrophoresis (PFGE) has been regarded as the “gold standard” method for MRSA typing (4, 27), and recently, the application of analysis of the staphylococcal cassette chromosome *mec* (SCCmec) element (13, 21, 23), multilocus sequence typing (MLST) (8), and spa typing have brought further progress to epidemiological studies of MRSA (12, 19, 25).

Previous studies demonstrated that two major MRSA clones are prevalent in Asian countries. On the basis of MLST and SCCmec typing, sequence type 5 (ST5)-MRSA-SCCmec type II (ST5-MRSA-II) was found to be prevalent in South Korea and Japan, while ST239-MRSA-III was prevalent in other Asian countries (1, 2, 5, 17). However, since the number of MRSA isolates from three hospitals in China analyzed in the previous studies was very limited, the data do not represent the nationwide distribution of MRSA genotypes in China (1, 5, 17). Therefore, further study of more isolates and isolates from more centers is needed. In this study, a combination of molecular typing methods, including PFGE, spa typing, MLST, and SCCmec typing, was used to characterize a collection of 702 MRSA isolates from 18
teaching hospitals in 14 cities recovered between 2005 and 2006 to show the genetic background of MRSA strains in China.

MATERIALS AND METHODS

Bacterial isolates. A total of 702 nonduplicate MRSA isolates were collected from 18 teaching hospitals in 14 cities from January 2005 to October 2006. The number of isolates from each city is summarized in Table 1, and the study centers are listed in Acknowledgments. The isolates were recovered from several clinical sources, including the respiratory tract (n = 371), blood (n = 93), secretions (n = 44), drainage (n = 40), pus (n = 40), wounds (n = 34), abdominal fluid (n = 15), and other sources (n = 65). Thirty-five isolates were obtained from outpatients, 10 isolates were obtained from emergency departments, 50 isolates were obtained from intensive care units, and the others were obtained from inpatients. The isolates were collected from nationwide surveillance networks organized by the Peking Union Medical College Hospital. Each center was required to send 50 isolates at the central labora-
tory; thus, the number of isolates may vary among the centers. In vitro susceptibility tests were performed with all S. aureus isolates at the central laboratory. All isolates were confirmed to be MRSA by multiplex PCR for the detection of the mecA and femB genes (18). CA-MRSA was defined as described by Klevens et al. (16).

Antimicrobial susceptibility testing. Antimicrobial susceptibility profiles were determined by the agar dilution method on Mueller-Hinton agar, according to the guidelines of Clinical and Laboratory Standards Institute (formerly the NCCCLS) (22). The antiseptic agents tested included oxacillin (Sigma Chemical Co., St Louis, Mo.), clindamycin (Sigma), ciprofloxacin (Bayer AG, Leverkusen, Germany), chloramphenicol (Sigma), erythromycin (Sigma), gentamicin (Sigma), rifampin (rifampicin; Sigma), tetracycline (Sigma), trimethoprim-sulfamethoxazole (Sigma), and vancomycin (Sigma). Clinical and Laboratory Standards Institute breakpoints were used for MIC interpretation (6). S. aureus ATCC 29213 and Enterococcus faecalis ATCC 29212 were used as quality controls in each set of tests.

DNA extraction. DNA was extracted as described by Unal et al. (28). The DNA was used as the template in all PCR assays below.

Molecular typing methods. All 702 isolates were analyzed by SCCmec typing and Panton-Valentine leukocidin gene (pvl) gene detection. PFGE and spa typing were used to characterize 395 isolates in 2005, and in 2006, only spa typing was used for 307 isolates. One hundred two isolates were selected as representatives of each PFGE and spa type for MLST typing. To be specific, isolates that had the same PFGE pattern or spa type but different antibiotic resistance profiles or SCCmec types were chosen for MLST typing.

(i) SCCmec typing. The SCCmec types were determined by a multiplex PCR strategy, as described previously (23). Nontypeable (NT) types were defined as isolates showing unexpected fragments or lacking some fragments by multiplex PCR. International clones of SCCmec types I to V were used as quality controls.

(ii) Detection of pvl. pvl was detected by PCR, as described previously (20). The identity of the PCR products was confirmed by sequencing with an ABI 3700 sequencer.

(iii) PFGE. DNA extraction and Smal restriction were performed as described previously (14). A bacteriophage lambda DNA PFGE molecular size standard was included in each gel. The PFGE patterns were examined visually and were interpreted according to the criteria of Tenover et al. (27).

(iv) spa typing. spa typing was performed as described previously (12, 19). Purified spa PCR products were sequenced, and short sequence repeats were assigned by using the spa database website (http://www.ridom.de/spaserver). The spa complex was defined by visual analysis, whereby spa types with similar short sequence repeats were clustered into the complexes previously described by Ruppit et al. (25).

(v) MLST and data analysis. MLST was performed as described previously (8). PCR fragments were purified and sequenced with an ABI 3700 sequencer. The sequences available on the MLST website (http://www.mlst.net) for S. aureus, and the allelic number was determined for each sequence. Clustering of related STs, which were defined as clonal complexes (CCs), was determined by using the program eBURST (based upon related sequence types) (9).

(vi) Collection of clinical data. The medical records of all patients from Peking Union Medical College Hospital (n = 198) and those of patients with pvl-positive isolates (n = 16) and SCCmec type IVa isolates (n = 4) were reviewed by physicians. The following variables were collected: patient demographics (gender and age); ward transfer; underlying diseases; the length of time after admission.
that a sample for culture was obtained; the presence of an invasive device (e.g., a vascular catheter or a gastric feeding tube) at the time of admission; and a history of MRSA infection or colonization, surgery, hospitalization, dialysis, or residence in a long-term care facility in the 12 months preceding the culture.

RESULTS

SCCmec types. All of the 702 MRSA isolates were analyzed by SCCmec typing. Overall, four SCCmec types, namely, types I, II, III, and IVa, were found. The most common SCCmec type was type III, which accounted for 109 (109/702; 15.5%) of all isolates and which existed in 10 cities. SCCmec type II was identified to be prevalent in Dalian (56.7%) and Xi’an (90.9%). SCCmec type II increased in Dalian, Shanghai, and Hangzhou and decreased in Shenyang and Beijing. On the contrary, the prevalence of SCCmec type III correspondingly decreased or increased in these cities during the two study periods.

Antibiotic resistance profiles and PFGE types. The PFGE types of the MRSA isolates recovered in 2005 and their respective antibiotic resistance profiles are listed in Table 2. Overall, 24 PFGE types and 42 subtypes were obtained. Four PFGE types (types A, F, L, and M) were found to be the predominant types, constituting 49.4% (195/395), 23.5% (93/395), 9.9% (39/395), and 5.8% (23/395) of all isolates, respectively. PFGE type A existed in 12 cities, type F existed in 8 cities, and type L existed in 6 cities, while type M existed in 4 cities.

The PFGE types were generally associated with unique antibiotic resistance profiles, and these are illustrated in Table 2. PFGE type H, I, L, M, and P isolates had the same antibiotic resistance profile of resistance to tetracycline, erythromycin, clindamycin, gentamicin, and ciprofloxacin (the TEDGCI resistance profile). PFGE type A, B, D, and V isolates were additionally resistant to rifampin, while PFGE type F and G isolates were additionally resistant to chloramphenicol and trimethoprim-sulfamethoxazole but were susceptible to rifampin. PFGE type O, R, U, and W isolates had the same antibiotic resistance profiles, and these are illustrated in Table 2.
tested were susceptible to vancomycin, but a shift in the MIC was identified. In 2005, the vancomycin MIC₉₀ was 0.5 mg/liter, while in 2006, the vancomycin MIC₉₀ increased to 1 mg/liter.

**spa types.** Typing of all isolates yielded 18 spa types (Table 3). The most predominant spa type was t030, which contained PFGE types A to K and G. spa type t037 accounted for 25.5% (179/702) of all isolates, and was present in all cities. The second common spa type t002, t570, and t601 isolates showed the same TEDGCi antibiotic resistance profile; and t002, t570, and t601 isolates showed the same TEDGCi antibiotic resistance profile; and t030, t632, and t1152 isolates presented additional resistance to rifampin. spa type t037 isolates had a profile of resistance to tetracycline, erythromycin, clindamycin, gentamicin, chloramphenicol, trimethoprim-sulfamethoxazole, and ciprofloxacin, while spa type t437 isolates were susceptible to gentamicin and had a profile of resistance to tetracycline, erythromycin, clindamycin, and ciprofloxacin.

The distribution of spa types varied among the cities (Table 4). spa type t002 was the most common spa type in Dalian (53.4%) and Shenyang (44.4%); spa type t037 was predominant in Shanghai (74.8%), Shenzhen, and Nanning; in the other cities, spa type t030 was the most common type. The second predominant spa type also showed different patterns of prevalence among the cities. The second most common spa type in Shanghai and Beijing was t002; that in Dalian, Hangzhou, and Xi’an was t037; and that in Shenyang and Guangzhou was t030.

**MLST analysis.** One hundred two isolates (53 isolates recovered in 2005, 49 isolates recovered in 2006) were selected for MLST analysis. The STs of representatives of the PFGE types or the spa types are presented in Table 2 and Table 3. Overall, eight STs were found among the 102 isolates. Clustering analysis by use of the eBURST program showed that these STs belonged to eight CCs. The most dominant ST was ST239, which belonged to CC239, constituted 80.8% (567/702) of all isolates, and existed in all cities. CC239 is a distinct branch within CC8. ST239 included PFGE types A to K and spa types t030, t037, t377, 459, t632, t803, and t1152. ST5, which belonged to CC5, was found to be the second common ST (117/702; 16.7%) and included PFGE types L to T and spa types t002, t570, and t601. The distribution of STs also exhibited different patterns among the cities. ST5 was the most predominant type in Shanghai and Beijing, while in Dalian, Hangzhou, and Xi’an was t037; and that in Shenyang and Guangzhou was t030.

<table>
<thead>
<tr>
<th>City</th>
<th>Total no. of isolates</th>
<th>% (no.) of isolates of the following spa type:</th>
</tr>
</thead>
<tbody>
<tr>
<td>Beijing</td>
<td>236</td>
<td>t030: 14.9% (35), t037: 76.7% (181), Other: 25.6% (57)</td>
</tr>
<tr>
<td>Chongqing</td>
<td>15</td>
<td>t030: 10.0% (3), t037: 12.0% (2), Other: 78.0% (13)</td>
</tr>
<tr>
<td>Dalian</td>
<td>30</td>
<td>t030: 10.0% (3), t037: 33.3% (10), Other: 56.7% (17)</td>
</tr>
<tr>
<td>Guangzhou</td>
<td>50</td>
<td>t030: 10.0% (3), t037: 40.0% (19), Other: 50.0% (18)</td>
</tr>
<tr>
<td>Hangzhou</td>
<td>58</td>
<td>t030: 10.0% (5), t037: 34.5% (20), Other: 55.5% (13)</td>
</tr>
<tr>
<td>Nanning</td>
<td>14</td>
<td>t030: 10.0% (4), t037: 34.5% (4), Other: 51.5% (6)</td>
</tr>
<tr>
<td>Nanning</td>
<td>8</td>
<td>t030: 10.0% (5), t037: 20.0% (3), Other: 60.0% (1)</td>
</tr>
<tr>
<td>Qingdao</td>
<td>30</td>
<td>t030: 10.0% (4), t037: 63.0% (19), Other: 23.3% (4)</td>
</tr>
<tr>
<td>Shanghai</td>
<td>103</td>
<td>t030: 10.0% (10), t037: 74.8% (77), Other: 15.2% (15)</td>
</tr>
<tr>
<td>Shenyang</td>
<td>54</td>
<td>t030: 10.0% (21), t037: 44.4% (24), Other: 16.7% (9)</td>
</tr>
<tr>
<td>Shenzhen</td>
<td>17</td>
<td>t030: 10.0% (13), t037: 30.0% (14), Other: 59.3% (2)</td>
</tr>
<tr>
<td>Xi’an</td>
<td>33</td>
<td>t030: 10.0% (23), t037: 49.4% (8), Other: 25.0% (2)</td>
</tr>
</tbody>
</table>

*The prevalence of spa types was not calculated in cities where the total number of isolates was less than 20.*
commonly identified ST in Dalian (16/30; 53.3%) and Shenyang (26/54; 48.1%), whereas ST239 was the most common ST identified in the other cities.

**Prevalence of pvl gene.** All the isolates were analyzed for the detection of the pvl gene; only 16 isolates were pvl positive (16/702, 2.3%). All 16 of these isolates were considered to be hospital-acquired MRSA (HA-MRSA), according to the information in the patients’ medical records (Table 5). In total, the most common species type was sputum (11/17; 68.8%).

**Detection of CA-MRSA.** Two isolates from Guangzhou without the pvl gene were confirmed to be CA-MRSA from the detailed clinical information. One isolate, which was resistant only to erythromycin, was characterized as ST59-MRSA-Iva and spa type t437, while the other isolate, which had a profile of resistance to erythromycin, clindamycin, and ciprofloxacin, belonged to ST88, harbored SCCmec type Iva, and had spa type t2649. However, one isolate from Changchun that had the genotype of ST88-MRSA-Iva and the pvl gene was confirmed from the clinical information to be a HA-MRSA isolate. Another isolate from Urumchi could not be identified as CA-MRSA because of a lack of adequate clinical data.

**DISCUSSION**

Elucidation of the mechanism of the geographic spread of MRSA has been greatly facilitated by the techniques of molecular epidemiology. Both spa typing and PFGE were performed in 2005; however, the previous study revealed that spa typing possessed significant advantages over PFGE in terms of speed, ease of interpretation, and exportability and was a reliable method for long-term, nationwide epidemiological surveillance studies (11), so we conducted spa typing instead of PFGE in 2006.

Previous studies have demonstrated that most HA-MRSA infections are due to a relatively small number of epidemic MRSA clones (7, 10). In Asia, the most popular clones are Brazil/Hungary (ST239-III) and New York/Japan (ST5-II) (1, 2, 5, 15, 17). The data from the present study confirm that these two clones with different spa types are spreading across China and have unique geographic distributions.

The most common clone found was ST239, which existed in all cities covering most areas in China, from Urumchi in the northwest to Shenzhen in the southeast. This clone included isolates with seven spa types, belonging to SCCmec type III with ST239, and had a profile of resistance to multiple drugs: tetracycline, erythromycin, clindamycin, gentamicin, and ciprofloxacin, with some isolates also being resistant to chloramphenicol, rifampin, and trimethoprim-sulfamethoxazole. In previous studies, data revealed that some isolates from mainland China belonged to this clone and were multidrug resistant (resistant to tetracycline, erythromycin, clindamycin, gentamicin, chloramphenicol, and ciprofloxacin) (1, 5, 17). The ST239-III group, which belongs to CC239 and which represents a distinct branch within CC8 in the evolutionary model of the emergence of MRSA (24), has been reported to be widespread in most areas in Asia except Japan and South Korea and in many countries worldwide (1, 2, 5, 17). This clone was also the most dominant one in Hong Kong (15), whereas ST241 (a single-locus variant of ST239) with SCCmec type III was prevalent in Taiwan (1). The second most predominant clone was ST5, which belonged to CC5. This clone existed in 12 cities and was also recovered from most areas across China, from Jilin in the north to Shenzhen in the south. This clone had three spa types, possessed SCCmec type II, and showed a TEDGCi multidrug resistance profile. This clone was common in Dalian, Shenyang, Shanghai, Beijing, and Hangzhou (it made up >10% of the isolates in each city). It was suggested that these isolates fell in the ST5-II group, which was derived from the same ancestor as the New York/Japan clone within CC5 (24). MRSA isolates of ST5 have spread widely in many countries worldwide and are the predominant clone in South Korea and

**TABLE 5. Characteristics of Panton-Valentine leukocidin-positive MRSA isolates**

<table>
<thead>
<tr>
<th>Isolate no.</th>
<th>Patient age (yr)</th>
<th>Specimen type</th>
<th>Algorithm</th>
<th>CIP</th>
<th>ERY</th>
<th>CLI</th>
<th>GEN</th>
<th>TET</th>
<th>RIF</th>
<th>CHL</th>
<th>SXT</th>
<th>VAN</th>
<th>SCCmec type</th>
<th>spa type</th>
<th>MLST type</th>
<th>CC</th>
</tr>
</thead>
<tbody>
<tr>
<td>BJ043</td>
<td>69</td>
<td>Abdominal drainage</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>II</td>
<td>030</td>
<td>ST239</td>
<td>8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>BJ068</td>
<td>33</td>
<td>Sputum</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>S</td>
<td>R</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>III</td>
<td>030</td>
<td>ST239</td>
<td>8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>BJ078</td>
<td>80</td>
<td>Sputum</td>
<td>R</td>
<td>R</td>
<td>S</td>
<td>R</td>
<td>S</td>
<td>R</td>
<td>S</td>
<td>S</td>
<td>III</td>
<td>030</td>
<td>ST239</td>
<td>8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>BJ082</td>
<td>86</td>
<td>Bile</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>III</td>
<td>030</td>
<td>ST239</td>
<td>8</td>
<td></td>
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</tr>
<tr>
<td>BJ085</td>
<td>89</td>
<td>Sputum</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>III</td>
<td>030</td>
<td>ST239</td>
<td>8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>BJ088</td>
<td>97</td>
<td>Sputum</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>S</td>
<td>S</td>
<td>III</td>
<td>030</td>
<td>ST239</td>
<td>8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>BJ210</td>
<td>58</td>
<td>Sputum</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>S</td>
<td>R</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>II</td>
<td>0002</td>
<td>ST5</td>
<td>5</td>
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<tr>
<td>BJ249</td>
<td>94</td>
<td>Sputum</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>S</td>
<td>S</td>
<td>III</td>
<td>030</td>
<td>ST239</td>
<td>8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>BJ250</td>
<td>40</td>
<td>Sputum</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>S</td>
<td>S</td>
<td>III</td>
<td>030</td>
<td>ST239</td>
<td>8</td>
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<td></td>
</tr>
<tr>
<td>BJ274</td>
<td>80</td>
<td>Sputum</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>S</td>
<td>S</td>
<td>III</td>
<td>030</td>
<td>ST239</td>
<td>8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>BJ363</td>
<td>74</td>
<td>Secretion</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>III</td>
<td>030</td>
<td>ST239</td>
<td>8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>BJ372</td>
<td>40</td>
<td>Sputum</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>S</td>
<td>S</td>
<td>III</td>
<td>030</td>
<td>ST239</td>
<td>8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>BJ390</td>
<td>75</td>
<td>Secretion</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>S</td>
<td>S</td>
<td>III</td>
<td>030</td>
<td>ST239</td>
<td>8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CC023</td>
<td>18</td>
<td>Sputum</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>S</td>
<td>S</td>
<td>III</td>
<td>030</td>
<td>ST239</td>
<td>8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>DL010</td>
<td>76</td>
<td>Sputum</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>II</td>
<td>030</td>
<td>ST5</td>
<td>5</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SZ009</td>
<td>45</td>
<td>Pus</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>S</td>
<td>S</td>
<td>R</td>
<td>S</td>
<td>III</td>
<td>037</td>
<td>ST37</td>
<td>8</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Notes:
- BJ, Beijing; CC, Changchun; DL, Dalian; SZ, Shenzhen. All isolates were HA-MRSA.
- CIP, ciprofloxacin; ERY, erythromycin; CLI, clindamycin; GEN, gentamicin; TET, tetracycline; RIF, rifampin, CHL, chloramphenicol; SXT, trimethoprim-sulfamethoxazole; VAN, vancomycin; R, resistant; S, susceptible.
Japan (5, 17). Interestingly, this clone was also found to be the second predominant one in Hong Kong (15).

CA-MRSA was most commonly implicated in skin and soft tissue infections and carried SCCmec type IV or V, as well as the pvl gene, in the majority of cases (20, 26, 29, 31). In this study, from the review of the patients’ medical records, we identified two isolates that were CA-MRSA. Both of them carried SCCmec type IVa and were from patients with skin infections, but they did not possess the pvl gene. It has been reported that CA-MRSA strains may spread in the hospital and cause nosocomial infections (26), but in this study, based on 18 hospitals across China, we did not identify this phenomenon.

In this study, 16 isolates harbored the pvl gene and belonged to three STs: ST239, ST5, and ST88. The clinical data demonstrated that all these isolates were obtained from patients with hospital-associated infections. Among these isolates, ST239 was the most predominant clone. These data may indicate that the sporadic Panton-Valentine leukocidin-positive isolates classified as HA-MRSA exist in Chinese hospitals but in a low proportion. Nevertheless, the risk of the emergence of Panton-Valentine leukocidin-positive HA-MRSA clones is an issue of concern and could result in the emergence of multidrug-resistant HA-MRSA isolates with increased virulence. Further investigation of the prevalence of carriage of pvl among CA-MRSA isolates is necessary.

There may be some limitations to this study. As it was a retrospective study, the medical records from emergency department patients and outpatients and from other hospitals was hard to obtain, and some of the data obtained may not have been able to provide enough information to entitle the isolates to be classified as CA-MRSA, so this study is just the tip of the iceberg on the prevalence of CA-MRSA. Because there are few studies on the prevalence of CA-MRSA in mainland China, a prospective study that includes accurate clinical data and more isolates and that uses the techniques of molecular epidemiology is needed.

In summary, our study documented that two major pan-MRSA clones (ST239 and ST5) have spread across China and have unique geographic distributions. Further study of CA-MRSA isolates should be conducted to elucidate the current status of CA-MRSA in China.

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References


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