Changing Molecular Epidemiology of Methicillin-Resistant *Staphylococcus aureus* Bloodstream Isolates from a Teaching Hospital in Northern Taiwan

Yhu-Chering Huang,1,2* Lin-Hui Su,2,3 Tsu-Lan Wu,2,3 and Tzou-Yien Lin1,2

Division of Pediatric Infectious Diseases, Chang Gung Children’s Hospital,1 School of Medicine, Chang Gung University,2 and Department of Clinical Pathology, Chang Gung Memorial Hospital,3 Taoyuan, Taiwan

Received 12 April 2006/Accepted 12 April 2006

A changing molecular epidemiology of methicillin-resistant *Staphylococcus aureus* (MRSA) bloodstream isolates from a university-affiliated hospital in Taiwan during a 4-year interval was demonstrated. The changing epidemiology is due to the introduction of a new epidemic clone (sequence type 5) and a local community clone (sequence type 59) of MRSA into the hospital.

In Taiwan, methicillin-resistant *Staphylococcus aureus* (MRSA) accounted for 53% to 83% of all *S. aureus* clinical isolates in 12 major hospitals in the year 2000 (10). In Chang Gung Memorial Hospital, about 70% of all *S. aureus* clinical isolates were methicillin resistant in the past decade. A molecular epidemiology analysis of MRSA clinical isolates performed during 2000 to 2001 identified a predominant genotype, designated as type A, which was similar to the Brazilian or Hungarian clone, in 79% of the 107 MRSA clinical isolates from our hospital (14). Recently, community-acquired MRSA colonization and infection emerged and were frequently seen in children without identifiable risk factors in Taiwan (3, 4, 9, 11, 12, 21). To evaluate the impact of community strains on nosocomial infections, we conducted this study by comparing the molecular characteristics of MRSA bloodstream isolates collected in our hospital over a 4-year interval.

A total of 124 MRSA bloodstream isolates (no duplicate strain from a single patient) were selected (1 per 10 consecutive isolates) from the stocks of our microbiology laboratory during each study period, which included October 2004 through June 2005 and August 2000 through September 2001. Identification of MRSA was confirmed according to the guidelines of the National Committee for Clinical Laboratory Standards (now Clinical and Laboratory Standards Institute) (16). Pulsed-field gel electrophoresis (PFGE) was performed according to the procedure described previously (13, 14). Strains with banding patterns that differed by four or more bands were considered different and were assigned to separate types. The presence of the Panton-Valentine leukocidin (PVL) gene was determined by a PCR assay described elsewhere (15). Multilocus sequence typing (MLST) was performed for selected strains of representative PFGE patterns as described elsewhere (7).

Table 1 illustrates the detailed distribution of PFGE patterns, MLST and SCCmeC types, and the presence of the PVL gene among all isolates during the two study periods. During 2000 to 2001, six PFGE patterns, designated types A, B, C, D, F, and AN, were identified and types A and C accounted for 78% and 14.5% of 124 isolates, respectively. During 2004 to 2005, 12 PFGE patterns (designated types A, B, C, D, F, AH, AA, AG, AJ, AK, AL, and AM) were identified. Types A and C, though still the two most common types, accounted for 31% and 17% of 124 isolates, respectively. There were four additional types (designated types B, F, and AH) that accounted for more than 10% (10.5% to 12.1%) of the 124 isolates, respectively.

Among the 24 isolates selected for MLST analysis, four sequence types (STs 239, 241, 59, and 5) accounted for all but two isolates. Sequence type 241 is a single-locus variant of ST239. All but one isolate of PFGE types A and B were characterized as SCCmeC III or its variant, IIIA, with the PVL gene absent, and only STs 239 and 241 were found in these isolates. In contrast, ST59 was predominantly found in PFGE types C and D; however, most isolates of type C were characterized as SCCmeC IV with the PVL gene absent, while most isolates of type D were characterized as SCCmeC Vp with the PVL gene present. All 30 isolates of PFGE types F and AH were characterized as SCCmeC II with the PVL gene absent, and only ST5 was found in these isolates.

Results from this study clearly indicate that the molecular epidemiology of clinical MRSA bloodstream isolates in a teaching hospital had been changing during the 4-year interval between the two periods. During the first study period, 78% of the isolates clustered in one major genotype, which was designated type A (ST239 or ST241; SCCmeC type III or its variant, IIIA, with the PVL gene absent) and was similar to the Brazilian or
Hungarian clone. During the second period, genotype A, though still the predominant type, accounted for only 31% of the isolates. The remaining isolates were evenly distributed in the other five PFGE genotypes but clustered in two sequence types (ST5 and ST59).

Previous studies (1, 6, 9, 20) regarding the molecular epidemiology of MRSA in Taiwan between 1992 and 2001 indicated that a major clone, which was similar to genotype A in the current study (ST239 or ST241), prevailed in Taiwan and accounted for 54% to 93% of clinical isolates from different hospitals islandwide. These findings suggested that the MRSA clone of ST239 or ST241 appeared to have prevailed in our hospital and even across the whole island during the last decade in Taiwan; however, the predominance was decreasing, and this clone might be replaced by other clones in the near future.

The major change between the two study periods was the emergence of the clone of ST5, which accounted for only one isolate in the first period but expanded to 23% of the isolates in the second period. The clone of ST5-SCCmec II was among the five epidemic clonal complexes worldwide and has spread in Japan, the United States, the United Kingdom, Finland, Ireland, etc. (8, 18). The MRSA clone of ST59 is considered to be a community clone in Taiwan (5, 19), and two major PFGE patterns (C and D) were identified in this study. The clone of designated genotype C-SCCmec IV, which accounted for around 15% of the isolates during both study periods, has even spread to San Francisco, Calif. The clone of designated type D (similar to PFT USA 1000 [2])-SCCmec type V7 with a PVL gene present in the current study was the community-associated clone in Taiwan (2), and the number of bloodstream isolates of this genotype did increase around 10% during the 4-year interval in our hospital, suggesting that the community strain was returning to the health care institutes.

Conclusively, a changing molecular epidemiology of MRSA clinical isolates during a 4-year interval has been demonstrated in a teaching hospital in northern Taiwan. The changing epidemiology seemed to be due to the introduction of both a new epidemic clone (ST5) and a local community clone (ST59) of MRSA into our hospital during this period. This changing molecular epidemiology should be monitored further.

This study was supported by a grant from Chang Gung Memorial Hospital (CMRP33128).

REFERENCES


15. NCCLS. 2000. Performance standards for antimicrobial disk diffusion sus-

---

### TABLE 1. Comparison of the distributions of PFGE patterns, MLST and SCCmec types, and the presence of PVL genes among 248 methicillin-resistant Staphylococcus aureus bloodstream isolates during the two study periods

<table>
<thead>
<tr>
<th>PFGE pattern</th>
<th>No. of PFGE subtypes</th>
<th>MLST type(s)</th>
<th>SCCmec type(s)</th>
<th>PVL gene</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>20</td>
<td>239 (5/6), 241 (1/6)</td>
<td>III (118), IIIA (17)</td>
<td>Absent (135)</td>
</tr>
<tr>
<td>B</td>
<td>13</td>
<td>239 (1/2), 241 (1/2)</td>
<td>III (15), IIIA (2), IV (1)</td>
<td>Absent (18)</td>
</tr>
<tr>
<td>C</td>
<td>16</td>
<td>59 (3/3)</td>
<td>IV (3), VT (13)</td>
<td>Absent (15)</td>
</tr>
<tr>
<td>D</td>
<td>7</td>
<td>59 (3/3)</td>
<td>IV (3), VT (1)</td>
<td>Absent (135)</td>
</tr>
<tr>
<td>F</td>
<td>8</td>
<td>5 (2/2)</td>
<td>Absent (16)</td>
<td></td>
</tr>
<tr>
<td>AH</td>
<td>6</td>
<td>5 (1/1)</td>
<td>Absent (14)</td>
<td></td>
</tr>
<tr>
<td>Other</td>
<td>8</td>
<td>508 (1/7)</td>
<td>Absent (3)</td>
<td></td>
</tr>
</tbody>
</table>

* Numbers in parentheses represent no. of isolates with this MLST type/no. with this PFGE pattern that underwent MLST analysis.

---


