Comment on: A survey of community-associated methicillin-resistant Staphylococcus aureus in Korea

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Keywords: S. aureus, epidemiology, MRSA

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Sir,

Studies on the molecular epidemiological characteristics of methicillin-resistant Staphylococcus aureus (MRSA) have demonstrated their genetic and geographic diversity in comparisons between the community-associated (CA) and hospital-associated (HA) strains. In addition, it has been suggested that the CA-MRSA found in Korea is genetically different from those found in other regions of the world.1–3 Recently, Kim et al.1 reported a nationwide survey of CA-MRSA in Korea. We also published an article on the same subject in Korea.4 Both studies confirmed the unique features of the Korean MRSA strains.

Kim et al.1 designed a prospective sentinel hospital laboratory-based survey from seven hospitals in Korea. After dividing the strains into CA-MRSA and HA-MRSA, 72 isolates from each group were compared. Pathogens, colonizers and an ‘undetermined’ group were all included in the study. However, we have collected isolates from blood, wounds and pus from six hospitals in an effort to exclude possible colonization and contaminants.5 The enrolled hospitals did not overlap in the two articles.1,2 The definitions of CA-MRSA and multidrug resistance (MDR), and the number of antibiotics used in susceptibility testing, were slightly different in comparisons between the two articles.1,2 Kim et al.1 calculated the resistance rate as the number of intermediate and resistance strains over the total number of strains. In contrast, we did not consider ‘intermediate’ as resistance.2 Finally, we clustered MRSA isolates into representative groups based on genetic backgrounds, and clonal types were redefined according to staphylococcal chromosome cassette mec (SCCmec) type and susceptibilities. Despite these differences, both articles demonstrated similar features of the MRSA in Korea: SCCmec type IVA/ST72/Panton–Valentine leucocidin (PVL)-negative and SCCmec type II or III/ST5 or ST239/PVL-negative strains were predominant in CA-MRSA and HA-MRSA, respectively.1,2 Kim et al.1 reported that for CA-MRSA, the prevalence of SCCmec type IVA was 43% and the prevalence of ST5 or ST239 was 35%, and that for HA-MRSA, the prevalence of SCCmec type II or III was 82% and the prevalence of ST5 or ST239 was 86%. Similarly, our data showed that for CA-MRSA, the prevalence of SCCmec type IVA was 53.1% and the prevalence of ST72 was 27.2%, and that for HA-MRSA, the prevalence of SCCmec type II or III was 73.6% and the prevalence of ST5 or ST239 was 73.7%.2 PVL toxin was rarely identified in either study.1,2 In Korea, SCCmec type II or III/ST5 or ST239 was prevalent in HA-MRSA.4,5 The articles by Kim et al.1 and Park et al.2 elucidated the characteristics of CA- and HA-MRSA in Korea. It is interesting that both studies were nationwide studies performed at the same time and had very similar results. We think the data shown in these articles1,2 represent the current features of both CA- and HA-MRSA in Korea.

However, we would like to recommend caution with regard to the conclusion that MDR in CA-MRSA was high (64%), as suggested by Kim et al.1 Jung et al.3 also reported that 60.7% of the CA-MRSA isolates were MDR. However, most of their CA-MRSA (82%) were community-onset HA-MRSA cases based on the definition of Kim et al.1 Another study in Korea6 showed that <50% of the strains, among 20 SCCmec type IVA, were MDR when standardized according to the definition of Kim et al.1 After conforming to the definitions of Kim et al.,1 we re-analysed our data and found that the overall MDR rate, in CA-MRSA, was 51.9%. However, we grouped the clonal types according to their genetic backgrounds and SCCmec type, and found antibiotic susceptibility patterns more distinctly classified (Table 1; modified from Park et al.7). For example, most ST72 belonging to B-I were not MDR. B-I, D-I and E-I corresponded to SCCmec type IVA, and most of B-I and D-I were not MDR either. Therefore, the SCCmec type IVA/ST72/PVL-negative clones, the dominant CA-MRSA strains in Korea, were not MDR at least. The clonal types could have the advantage of demonstrating antibiotic susceptibility patterns more precisely than the groups defined by SCCmec only. We agree with Kim et al.1 and Jung et al.3 that there were multiple clones of CA-MRSA circulating in communities in Korea and some clones had MDR characteristics similar to HA-MRSA. Even in the dominant SCCmec type IVA in CA-MRSA, our data showed that there would be at least three different groups; however, only 30.2% were MDR.2 As commented on by Park et al.,2 isolates classified as ‘undetermined’ (46.4%) were all recovered from patients with chronic otitis media; most of them belonged to ST5 or ST239, which was predominant in the HA-MRSA. These findings may explain why the authors concluded that the MDR rate was high in the CA-MRSA. If the subgroup analysis was performed for the pathogen, colonizer and undetermined groups, or the clonal type was used in the analysis, a different conclusion would be expected. In order to confirm the epidemiological characteristics, standardization of study design, classifications and definitions are required. Further study is required to monitor the current trends and detect changes when they occur both locally and worldwide.

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Letters to the Editor

Table 1. Antimicrobial susceptibilities of community-associated (n = 81) methicillin-resistant Staphylococcus aureus (CA-MRSA) isolates based on clonal type\(^1\); number (%) of susceptible isolates

<table>
<thead>
<tr>
<th>CA-MRSA [n (%)]</th>
<th>A-I (n = 6)</th>
<th>A-II (n = 7)</th>
<th>B-I(^b) (n = 21)</th>
<th>C-I (n = 7)</th>
<th>C-II (n = 5)</th>
<th>D-I(^b) (n = 21)</th>
<th>E-I(^b) (n = 7)</th>
<th>others(^c) (n = 7)</th>
<th>total (n = 81)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Erythromycin</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>10 (47.6)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>2 (9.5)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>12 (14.8)</td>
</tr>
<tr>
<td>Clindamycin</td>
<td>1 (16.7)</td>
<td>0 (0.0)</td>
<td>21 (100)</td>
<td>2 (28.6)</td>
<td>1 (20.0)</td>
<td>21 (100)</td>
<td>1 (14.3)</td>
<td>5 (71.4)</td>
<td>52 (64.2)</td>
</tr>
<tr>
<td>Ciprofloxacin</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>21 (100)</td>
<td>0 (0.0)</td>
<td>1 (20.0)</td>
<td>21 (100)</td>
<td>7 (100)</td>
<td>6 (85.7)</td>
<td>56 (69.1)</td>
</tr>
<tr>
<td>Gentamicin</td>
<td>1 (16.7)</td>
<td>0 (0.0)</td>
<td>16 (76.2)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>1 (14.3)</td>
<td>3 (29.2)</td>
</tr>
<tr>
<td>Rifampicin</td>
<td>6 (100)</td>
<td>7 (100)</td>
<td>21 (100)</td>
<td>7 (100)</td>
<td>4 (80.0)</td>
<td>21 (100)</td>
<td>7 (100)</td>
<td>7 (100)</td>
<td>80 (98.8)</td>
</tr>
<tr>
<td>SXT</td>
<td>6 (100)</td>
<td>7 (100)</td>
<td>21 (100)</td>
<td>7 (100)</td>
<td>5 (100)</td>
<td>21 (100)</td>
<td>7 (100)</td>
<td>7 (100)</td>
<td>74 (91.4)</td>
</tr>
<tr>
<td>Tetracycline</td>
<td>0 (0.0)</td>
<td>6 (85.7)</td>
<td>21 (100)</td>
<td>0 (0.0)</td>
<td>1 (20.0)</td>
<td>9 (42.9)</td>
<td>7 (100)</td>
<td>7 (100)</td>
<td>51 (63.0)</td>
</tr>
<tr>
<td>Vancomycin</td>
<td>6 (100)</td>
<td>7 (100)</td>
<td>21 (100)</td>
<td>7 (100)</td>
<td>5 (100)</td>
<td>21 (100)</td>
<td>7 (100)</td>
<td>7 (100)</td>
<td>81 (100)</td>
</tr>
</tbody>
</table>

SXT, trimethoprim/sulfamethoxazole.

\(^a\)All strains of SCCmec type IVA were included in these three types.

\(^b\)Isolates of minor clonal types and the SCCmec NT group are included.

Transparency declarations

None to declare.

References


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Survey of community-associated methicillin-resistant Staphylococcus aureus in Korea—authors’ response

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Keywords: S. aureus, CA-MRSA, multidrug resistance

Sir,

We thank Park et al.\(^1\) for their thoughtful comments on our study on community-associated methicillin-resistant Staphylococcus aureus (CA-MRSA) in Korea.\(^2\) We agree that our finding of multidrug-resistant (MDR) CA-MRSA should be interpreted with caution. When we re-analysed our data on antibiotic resistance according to the clinical significance of the CA-MRSA isolates, the MDR rate was 47% in the pathogen group, 38% in the colonizer group and 97% in the group of undetermined significance (Table 1). The rates of MDR were also very different depending on the sequence types (STs) of the CA-MRSA isolates. For instance, only 1 of 25 isolates of the ST72 clone was MDR, whereas all the isolates of the ST5 and ST239 clones were MDR. Of the 31 isolates of the staphylococcal cassette chromosome mec (SCCmec) IVa clone, 8 (26%) were MDR.

Even though all of our isolates met the definition of CA-MRSA,\(^3\) we cannot exclude the possibility that some were actually hospital-associated, as we mentioned in the Discussion section of the previous study.\(^2\) To rule out this possibility, we also re-calculated the MDR rate after excluding the isolates of the ST5 and ST239 clones, the two most prevalent clones...