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

Chulmin Park, Dong-Gun Lee*, Su-Mi Choi, Jung-Hyun Choi, Sun Hee Park, Jin-Hong Yoo and Wan-Shik Shin

Department of Internal Medicine, College of Medicine, The Catholic University of Korea, Seoul 150-713, Korea

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*Corresponding author. Tel: +82-2-590-2494; Fax: +82-2-535-2494; E-mail: symonlee@catholic.ac.kr

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.4 reported a nationwide survey of CA-MRSA in Korea. After conforming to the definitions of Kim et al.1 and Park et al.,2 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.). 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; number (%) of susceptible isolates

<table>
<thead>
<tr>
<th>Clonal Type</th>
<th>CA-MRSA [n (%)]</th>
</tr>
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<tbody>
<tr>
<td>A-I (n=6)</td>
<td>A-II (n=7)</td>
</tr>
<tr>
<td>Erythromycin</td>
<td>0 (0.0)</td>
</tr>
<tr>
<td>Clindamycin</td>
<td>1 (16.7)</td>
</tr>
<tr>
<td>Ciprofloxacin</td>
<td>0 (0.0)</td>
</tr>
<tr>
<td>Gentamicin</td>
<td>1 (16.7)</td>
</tr>
<tr>
<td>Rifampicin</td>
<td>6 (100)</td>
</tr>
<tr>
<td>SXT</td>
<td>6 (100)</td>
</tr>
<tr>
<td>Tetracycline</td>
<td>0 (0.0)</td>
</tr>
<tr>
<td>Vancomycin</td>
<td>6 (100)</td>
</tr>
</tbody>
</table>

Erythromycin: 0 (0.0) | Clindamycin: 1 (16.7) | Ciprofloxacin: 0 (0.0) | Gentamicin: 1 (16.7) | Rifampicin: 6 (100) | SXT: 6 (100) | Tetracycline: 0 (0.0) | Vancomycin: 6 (100) |

SXT, trimethoprim/sulfamethoxazole.

*Table modified from Park et al.*

**Transparency declarations**

None to declare.

**References**


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

Eu Suk Kim1, Hong Bin Kim2,3* and Myoung-don Oh2

1Department of Internal Medicine, Dongguk University College of Medicine, Goyang, Republic of Korea; 2Department of Internal Medicine, Seoul National University College of Medicine, Seoul, Republic of Korea; 3Department of Internal Medicine, Seoul National University Bundang Hospital, Seongnam, Republic of Korea

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

Sir,

We thank Park et al.'s thoughtful comments on our study on community-associated methicillin-resistant Staphylococcus aureus (CA-MRSA) in Korea. 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, we cannot exclude the possibility that some were actually hospital-associated, as we mentioned in the Discussion section of the previous study. 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.