Community-associated Methicillin-resistant Staphylococcus aureus, Singapore

To the Editor: Community-associated methicillin-resistant Staphylococcus aureus (CA-MRSA) is an emerging phenomenon that has been reported from almost every continent in the world (1–4). Such strains are usually characterized by multisusceptibility to non-β-lactam antimicrobial drugs, production of Panton-Valentine leukocidin (PVL), and presence of staphylococcal chromosome cassette mec (SCCmec) IVa, a novel smaller variant of the methicillin-resistance locus (5). The genetic backgrounds of CA-MRSA strains from different parts of the world are distinct and specific for each geographic region (1–5).

We conducted a study at our institution, a 1,600-bed adult acute-care, tertiary-level public hospital, to determine evidence and the clinical and molecular profile of CA-MRSA in Singapore. We reviewed the microbiology laboratory records at our institution for multidrug-susceptible MRSA strains isolated from January 1, 2001, to April 15, 2004. S. aureus was identified by colony morphologic features, coagulation of citrated rabbit plasma with EDTA (BBL Becton Dickinson and Co., Cockeysville, MD, USA), and production of clumping factor and protein A (BactiStaph, Remel, Lenexa, KS, USA). Methicillin resistance was determined by susceptibility testing and confirmed by latex agglutination for penicillin binding protein-2a (6). Multidrug-susceptible strains were defined by susceptibility testing in terms of toxin profile and PFGE patterns were also performed in France; the latter was achieved by using Taxotron software (Institut Pasteur, Paris, France) to digitize and analyze SFML macrorestriction patterns.

Eight of 266 multidrug-susceptible strains fulfilled the criteria for community acquisition, but only 5 of these strains (corresponding to patients 1, 3, and 6–8) had been archived. The demographic and clinical data of the patients are shown in the Table. Most were young, healthy adults with cutaneous abscesses. Patient 1 had diabetes mellitus but had never been hospitalized; he was the only patient with severe bacteremic pneumonia. Patient 6 had early-stage endometrial cancer resected in 2000 but had not attended her follow-up appointments for >1 year before her hospitalization. Patient 8 had traveled to Taipei,

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Table. Demographic and clinical data of patients with community-associated methicillin-resistant Staphylococcus aureus (MRSA)

| Patient | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 |
|---------|---|---|---|---|---|---|---|---|
| Date of MRSA isolation | Mar 2001 | Nov 2002 | Jan 2003 | Feb 2003 | Mar 2003 | May 2003 | Oct 2003 | Apr 2004 |
| Ethnicity | Indian | Filipino | Chinese | Chinese | Filipino | Chinese | Filipino | Chinese |
| Age | 52 | 20 | 38 | 37 | 31 | 56 | 21 | 33 |
| Sex | M | F | M | M | F | F | F | F |
| Coexisting conditions | Diabetes mellitus | – | – | – | – | Endometrial cancer | – | – |
| Infection type | Pneumonia, bacteremia | Hand abscess | Hand abscess | Hand abscess | Hand abscess | Hand abscess | Hand abscess | Hand abscess |
| Therapy* | IV vancomycin | i&d | i&d | i&d | i&d | i&d | i&d | i&d |
| Appropriate antimicrobial drug usage | Yes | No | No | No | No | No | No | No |

*Therapy: IV, intravenous; –, not applicable; i&d, incision and drainage of abscess.
Taiwan, for a month; the abscess developed 3 days after her return home. Travel history was not documented in the other patients’ records. Patients 2–8 received β-lactam antimicrobial drugs in addition to surgical drainage of their abscesses and recovered without any complications.

All 5 archived strains had different molecular and toxin profiles, and the only consistent feature was the presence of PVL genes. Isolates 3 and 7 possessed SCCmec IV. Isolates 1, 6, and 8 were mecA positive, but their SCCmec belonged to none of the 4 major structural types. Comparisons with published data on CA-MRSA strains showed that isolate 7 was identical to the European strain of CA-MRSA in terms of PFGE pattern, toxin profile, and sequence type (ST 80) (2,5). Isolate 3 had an identical PFGE pattern and sequence type (ST 30) compared to the Oceanian Southwest Pacific strain but differed slightly in toxin profile, as the LukD-LukE leukocidin genes were absent (3,5). Isolate 8 was similar to the Taiwanese strains: it was ST 59 and had non-typable SCCmec (4). It belonged to agr 1 and tested positive for enterotoxin sek, γ2-hemolysin, and β-hemolysin genes.

Isolate 6 had a PFGE pattern that may be distantly related to U.S. strains; the similar sequence type (ST 1) served to emphasize this, although the presence of nontypable SCCmec rather than SCCmec IV implied that methicillin resistance was acquired differently. It belonged to agr 3 and tested positive for LukD-LukE leukocidin, enterotoxins seb and seh, and γ2-hemolysin genes. Isolate 1 is unique to Singapore in that it had a novel sequence type (ST524: 7-6-1-5-71-5-6 and SCCmec). It belonged to agr 1 and tested positive for γ-hemolysin gene as well as for the enterotoxin gene cluster.

Widely diversified CA-MRSA strains exist in Singapore. The demographic profile and clinical symptoms of local patients infected with these strains were consistent with published literature (2–4). The lack of a pediatric unit at our institution prevented a more complete epidemiologic description.

In contrast to previous reports (1–5), our findings are unique in that most of our strains do not have a distinctive molecular profile and may be related to strains from different parts of the world. Epidemiologic and molecular data strongly suggest that isolate 8 was imported from Taiwan. Some of the other strains (especially isolates 3 and 7) may have been imported from other countries too, as Singapore is an international travel hub with >6 million visitors annually.

CA-MRSA has only been isolated sporadically in Singapore, and no dominant clone was seen among our isolates. Singapore may be in an early phase of CA-MRSA emergence, and healthcare workers should remain vigilant for future outbreaks.

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Li-Yang Hsu,* Anne Tristan,† Tse-Hsien Koh,* Michèle Bes,† Jerome Etienne,† Asok Kurup,* Thuan-Tong Tan,* and Ban-Hock Tan*  
*Singapore General Hospital, Singapore; †Faculté de Médecine Laënnec, Lyon, France

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Address for correspondence: Li-Yang Hsu, Department of Internal Medicine, Singapore General Hospital, Outram Rd, S169608, Singapore; fax: 65-67322601; email: liyang_hsu@yahoo.com