Diversity in the antimicrobial susceptibility patterns of methicillin-resistant *Staphylococcus aureus* clones

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Received: 19 June 2012 / Accepted: 9 July 2012 / Published online: 25 July 2012 © Springer-Verlag 2012

**Abstract** Methicillin-resistant *Staphylococcus aureus* (MRSA) is well known for its epidemicity, with the emergence of new clones on a daily basis. Diversity in the clonal types of MRSA challenges the success of treatment, as different clones respond to different sets of antibiotics. However, the antibiotic susceptibility among the isolates within the same clones is largely unexplored. In a previous study on MRSA epidemiology in Malaysia, we identified six major clonal complexes (ST-239-CC8, ST-1-CC1, ST-188-CC1, ST-22-CC22, ST-7-CC7 and ST-1283-CC8). In the present study, we investigated the antibiotic susceptibility patterns of isolates of different clones. Three hundred and eighty-nine MRSA isolates were subjected to the disc diffusion test, oxacillin minimum inhibitory concentration (MIC) determination and assessment of the distribution of macrolide, lincosamide and streptogramin B (MLSb) resistance genes. Thirty-six different antibiotic profiles were observed: 30 (83.3 %) among ST-239, 2 (5.6 %) among ST-1283 and 1 (2.8 %) each for ST-1, ST-7, ST-22 and ST-188. All ST-239 (362, 9 %) isolates were multiple drug-resistant (MDR; resistant to more than three classes of antibiotics) and had oxacillin MICs >256 mg/l. Among the 385 clindamycin-resistant isolates, 375 (96.4 %) illustrated inducible resistance (D-zone-positive), while 10 (2.6 %) showed constitutive resistance. The vast majority of the macrolide-resistant isolates carried the *ermA* gene (95.1 %), followed by *ermC* (12.9 %). Diversity in the antibiotic susceptibilities of isolates within the clones emphasises the need for continuous surveillance of MDR strains to prescribe the correct antibiotic rather than empirical treatment. This will likely reduce the emergence of new endemic or epidemic resistant MRSA clones.

**Introduction**

Methicillin-resistant *Staphylococcus aureus* (MRSA), which is one of the top nosocomial pathogens, causes a...