A low prevalence of inducible macrolide, lincosamide, and streptogramin B Resistance phenotype among methicillin-susceptible staphylococcus aureus isolated from Malaysian patients and healthy individuals

ABSTRACT

Background: Antibiotic resistance among Staphylococcus aureus is of great concern worldwide. This resistance is further complicated by the ability of S. aureus to confer cross-resistance to other antibiotics due to the presence of resistance genes, such as erythromycin resistance methylase (erm) genes, which render the bacterium resistant to macrolide-lincosamide-streptogramin B (MLSB) antibiotics. Resistance to these antibiotics can lead to therapeutic failure, resulting in significant morbidity and mortality in patients with S. aureus infections. **Objectives**: This study was performed to examine the distribution of MLSB-resistant strains of methicillin-susceptible S. aureus (MSSA), which were obtained from hospitalized patients and normal healthy individuals (carriers) using phenotypic methods, such as the double-disk diffusion (D-test) and the genotypic method by polymerase chain reaction (PCR). **Methods**: A total of 183 nonduplicative MSSA isolates obtained from hospitalized patients (133) and carriers (50) in our previous studies were randomly selected for the D-test. The guidelines of the Clinical and Laboratory Standards Institute (CLSI) were used for the interpretation of the results of this test. The detection of ermA, ermB, ermC and msrA genes by PCR was performed for isolates that had positive D-test results and that were resistant to erythromycin. **Results**: Of the 183 MSSA isolates, 97.2% and 98.4% were highly susceptible to erythromycin and clindamycin, respectively. MSLB resistance was detected in four isolates (2.2%). Of the 133 MSSA isolated from hospitalized patients, only 3.0% (4/133) and 2.3% (3/133) exhibited resistance to erythromycin and clindamycin, respectively. With regard to the MLSB resistance phenotypes, only 1.6% and 0.6% exhibited inducible MLSB (iMLSB) and MS phenotypes, respectively. The ermC gene was detected in all three iMLSB phenotypes, and the msrA gene was detected in the MS phenotype. Surprisingly, all MSSA isolates (100%) from carriers exhibited extremely high susceptibility to both antibiotics. **Conclusions**: The prevalence rates of iMLSB MSSA isolates vary according to geographical locations and the local antibiotic policy. The low prevalence rate of iMLSB MSSA isolates could probably be related to the judicious use of antibiotics for treating S. aureus infections in our studied population. Nonetheless, continuous antibiotic surveillance is still necessary to control any emergence of resistance isolates so that targeted therapy and effective control can be implemented accordingly.

Keyword: Erythromycin; Clindamycin; Resistance; Methicillin; *Staphylococcus aureus*