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Molecular analysis and frequency of *Staphylococcus aureus* virulence genes isolated from bloodstream infections in a teaching hospital in Tianjin, China

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ABSTRACT. *Staphylococcus aureus* is an important cause of bloodstream infections worldwide. We examined the prevalence of genes that encode erythromycin ribosome methylase and bacterial toxins in *S. aureus* collected from bloodstream infections. Sixty different *S. aureus* isolates were obtained from blood cultures of patients who were admitted to a Teaching Hospital in Tianjin from January 2006 to August 2011. The susceptibility of the isolates to 16 antibiotics was tested. Methicillin-resistant *S. aureus* (MRSA) was identified using the disk diffusion method with cefoxitin. PCR was used to detect genes that encode the staphylococcal enterotoxins, Panton-Valentine leukocidin, toxic shock syndrome toxin 1 and erythromycin ribosome methylase. Molecular analysis of the MRSA strains was done using pulsed-field gel electrophoresis (PFGE) and staphylococcal cassette chromosome mec (SCCmec) typing. The positivity rates of *mecA*, *ermA*, *ermB*, and *ermC* in the isolates were 13/60, 10/60, 18/60, and 18/60, respectively. Among the

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60 isolates, 30 harbored enterotoxin genes, with *sea* as the most frequent toxin gene (33%), followed by *sec* (15%), *sed* (12%), and *seb* (5%). The *see* and *tst* genes were not found in any of the isolates. The *pvl* gene was detected in four strains. Eleven MRSA isolates were of the SCCmec type III; two MRSA isolates could not be determined through SCCmec typing. PFGE analysis of the 13 MRSA isolates produced 8 distinct pulsotypes. Virulence genes and erythromycin ribosome methylase genes were highly prevalent in these isolates. The PFGE results demonstrated that the MRSA spread through cloning, mainly involving SCCmec type III.

Key words: *Staphylococcus aureus*; Bloodstream infections; Virulence gene; Erythromycin ribosome methylase gene

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