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Characterisation of the Virulence Factors and Genetic Types of Methicillin Susceptible Staphylococcus aureus from Patients and Healthy Individuals

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Abstract Methicillin sensitive Staphylococcus aureus is an important bacterial pathogen associated with hospital- and community-acquired infections leading to endocarditis, skin tissue infection and pneumonia. The objective of this study was to determine both the genetic characteristics of methicillin-sensitive S. aureus (MSSA) strains, and the occurrence of virulence factors produced by S. aureus strains isolated from UMMC and healthy students in the University from year 2009. Out of 429 nasal swab samples, 67 were MSSA. The prevalence of 21 different virulence genes among 67 Malaysian clinical and community MSSA strains was determined by PCR, and their genetic features were assessed by PCR-RFLP of coa gene, agr types, spa typing and PFGE. The five predominant virulence genes were ica (79 %), efb and fnbA (61 % each), sdrE (57 %) and hlg (45 %). Toxin genes (enterotoxin, etd and pvl) were significantly more common (P < 0.05) in clinical strains compared to community strains. Three agr genotypes were observed: agr type I (45 %), agr type II (25 %) and agr type II (19 %). All 67 MSSA strains were distinguished into 26 profiles by PCR-RFLP of coa, 55 pulstypes and 21 spa types. Four novel spa types (t7312, t7581, t7582 and t7583) were observed. In conclusion, different virulence profiles were observed in MSSA strains in Malaysia where toxin genes were more prevalent among clinical strains. No correlation between DNA profiles (coa-RFLP, PFGE and spa) and virulotypes was observed. The Malaysian MSSA strains from clinical and community sources were genetically diverse and heterogeneous.

Keywords Staphylococcus aureus · Virulence genes · PFGE · spa and agr

Introduction

Staphylococcus aureus is one of the most important bacterial pathogens responsible for food-borne poisoning and toxin-mediated disease [1]. It produces different types of virulence factors, which are involved in attachment, persistence, tissue penetration and sepsis [2].

Enterotoxins are short secreted proteins that are usually heat-resistant, and usually resistant to most of the proteolytic enzymes produced by the human body [3]. There are more than 20 different types of enterotoxins (SEA to SEE, SEG to SEI, SEI, SEI, SEI, SEI, SEI, SEI, SEI, SEI, SEI, SEI) being reported [4]. An accessory gene regulator (agr) is known to be a global regulator of staphylococcal virulon which coordinates the expression of secretion-and cell-associated virulence factors [5].

MRSA has evolved from methicillin-susceptible S. aureus (MSSA) via acquisition of mobile genetic elements called staphylococcal cassette chromosome mec (SCCmec) [6, 7]. Hence; MSSA is known to be a potential reservoir for these MRSA strains.

Several methods are available for subtyping S. aureus, include PCR-RFLP of coa gene [8], pulsed-field gel electrophoresis (PFGE) [9], and spa typing [10]. PCR-RFLP of