Molecular typing and virulence profiling of Staphylococcus aureus isolates from a non-tertiary hospital in South Korea

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Background: Staphylococcus aureus (S. aureus) is a major human pathogen associated with both nosocomial and community acquired infections. In South Korea, the spread of methicillin-resistant S. aureus (MRSA) is a problem in healthcare setting, but the genetic characteristics of S. aureus prevalent in non-tertiary hospitals and community have not been known yet. In this study, we investigated the characteristics of S. aureus isolated from non-tertiary hospitals.

Material/methods: S. aureus isolates recovered from clinical specimens in non-tertiary hospitals were collected from five laboratory centers during 2013-2014 as a part of National Antimicrobial Resistance Surveillance Project. Antimicrobial susceptibility test for all isolates was performed, and molecular types were characterized by MLST, SCCmec, agr, and spa typing. The virulence genes including Panton-Valentine Leukocidin (PVL) gene, toxin shock syndrome toxin 1 (TSST) gene, exfoliative toxins (ETs) and staphylococcal enterotoxins (SEs; SEA to SEE, SEG to SEJ) were identified by conventional PCR or multiplex DNA amplification.

Results: Among a total of 447 S. aureus isolates, 272 MRSA (60.9%) and 175 MSSA (39.1%) were identified. The 43 sequences types (STs) were determined by MLST (primarily ST72, ST5, ST239, ST188 and ST1) and 84 spa types were confirmed. The most frequent STs of MRSA isolates were ST5 (n=113), ST72 (n=83), and ST239 (n=27), while those of MSSA isolates were ST72 (n=39), ST188 (n=20) and ST1 (n=19). The 130 isolates (47.8%) of all MRSA isolates were SCCmec type II, 106 (39.0%) were SCCmec type IV, and 33 (12.1%) were SCCmec type III. The most prevalent combinations of enterotoxin genes in MRSA isolates were seg-sei (41.2%) and sec-seg-sei (34.2%), and the most of MRSA isolates containing sec-seg-sei harbored tsst gene (91.4%). Among all S. aureus isolates, 19 (4.3%) and 9 (2.0%) isolates were positive to PVL and ET genes, respectively.

Conclusions: This study suggests that ST5-SCCmec II-t2460 (16.2%), ST5-SCCmec II-t002 (12.5%), and ST72-SCCmecIV-t324 (11.0%) were predominant MRSA clones in non-tertiary hospitals in South Korea.